

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/564,277
Source: 1FwP
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RAW SEQUENCE LISTING DATE: 01/20/2006
PATENT APPLICATION: US/10/564,277 **TIME:** 12:11:10

Input Set : N:\SMITH\PTO.TAS19.txt
 Output Set: N:\CRF4\01202006\J564277.raw

3 <110> APPLICANT: Developen Aktiengesellschaft fur entwicklungsbiolo
 5 <120> TITLE OF INVENTION: Use of DG153 or DG177 secreted protein products for
 6 preventing and treating pancreatic diseases and/or
 7 obesity and/or metabolic syndrome
 9 <130> FILE REFERENCE: 31130PWO WWHC
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/564,277
 C--> 12 <141> CURRENT FILING DATE: 2006-01-11
 14 <150> PRIOR APPLICATION NUMBER: EP03015883.6
 15 <151> PRIOR FILING DATE: 2003-07-11
 17 <150> PRIOR APPLICATION NUMBER: EP03016710.0
 18 <151> PRIOR FILING DATE: 2003-07-22
 20 <160> NUMBER OF SEQ ID NOS: 11
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1103
 26 <212> TYPE: DNA
 27 <213> ORGANISM: human
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: nucleotide sequence of human DG153 protein
 32 <400> SEQUENCE: 1
 33 cttcggtcct gctgttagtgc ctctcgccaggcccggtt caatcagccg ccacaactgt 60
 34 cttagggctca gacaccacca gccaatgagg gagggcacgt ggagccgcgt ctgggctcgc 120
 35 ggctcctgac caatggggaa gtggcatgtg ggagggcgcc ggggttcccc cgcctaattgg 180
 36 ggagctacgg cgccgcggccg ggacttggag gcgggtgcggc gcggcggttgcggcgtc 240
 37 ggtcggcgccg ggcagccggag gaggaggagg aggaggagg tgaggaggat gaggaggatg 300
 38 tggccacgc aggggctggc ggtgcgcgtg gctctgagcg tgctgccggc cagccggcg 360
 39 ctgcggccgg ggcactgcga agttgtatt tcttatctgg gaagattta ccagacaccc 420
 40 aaagacagag atgtcacatt ctccaccaggcc actattgaaa acgaacttat aaagttctgc 480
 41 cgggaagcaa gaggcaaaga gaatcggtt tgctactata tcggggccac agatgatgca 540
 42 gccaccaaaa tcatcaatga ggtatcaaag cctctggccc accacatccc tgtggagaag 600
 43 atctgtgaga agcttaagaa gaaggacacgc cagatatgtg agcttaagta tgacaaggcag 660
 44 atcgaccctga gcacagtggc ctccgagttt aagagctgaa gaagattctg 720
 45 gatgactggg gggagacatg caaaggctgt gcagaaaagt ctgactacat ccggaaagata 780
 46 aatgaactga tgcctaaata tgcccccacag gcagccatg caccgaccga tttgtatct 840
 47 gctcaatctc ttttgcaccc gaggggggaaa aaacagttca actgttact cccaaaacag 900
 48 cctttttgtt atttattttt taagtggcgt cctgacaata ctgtatcaga tgtgaagcct 960
 49 ggagctttcc tcatgtatgtt ggccttacag tacccttcatg aggggattcc cttccttctg 1020
 50 ttgttgcgtt actctaggac ttcaaaatgtt gtctggatt ttttattaa agaaaaaaaaa 1080
 51 ttcttagctg tcaaaaaaaaaaaa aaa 1103
 54 <210> SEQ ID NO: 2
 55 <211> LENGTH: 234
 56 <212> TYPE: PRT
 57 <213> ORGANISM: human

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59 <220> FEATURE:
60 <223> OTHER INFORMATION: amino acid sequence of human DG153 protein, longer
61 variant
63 <400> SEQUENCE: 2
64 Met Gly Lys Trp His Val Gly Gly Arg Arg Gly Ser Pro Arg Gln Trp
65 1 5 10 15
66 Gly Ala Thr Ala Arg Gly Arg Asp Leu Glu Ala Val Arg Arg Gly Gly
67 20 25 30
68 Cys Gly Ser Val Gly Arg Arg Gln Arg Arg Arg Arg Arg Arg Arg Arg
69 35 40 45
70 Arg Met Arg Arg Met Arg Arg Met Trp Ala Thr Gln Gly Leu Ala Val
71 50 55 60
72 Arg Val Ala Leu Ser Val Leu Pro Gly Ser Arg Ala Leu Arg Pro Gly
73 65 70 75 80
74 Asp Cys Glu Val Cys Ile Ser Tyr Leu Gly Arg Phe Tyr Gln Asp Leu
75 85 90 95
76 Lys Asp Arg Asp Val Thr Phe Ser Pro Ala Thr Ile Glu Asn Glu Leu
77 100 105 110
78 Ile Lys Phe Cys Arg Glu Ala Arg Gly Lys Glu Asn Arg Leu Cys Tyr
79 115 120 125
80 Tyr Ile Gly Ala Thr Asp Asp Ala Ala Thr Lys Ile Ile Asn Glu Val
81 130 135 140
82 Ser Lys Pro Leu Ala His His Ile Pro Val Glu Lys Ile Cys Glu Lys
83 145 150 155 160
84 Leu Lys Lys Asp Ser Gln Ile Cys Glu Leu Lys Tyr Asp Lys Gln
85 165 170 175
86 Ile Asp Leu Ser Thr Val Asp Leu Lys Lys Leu Arg Val Lys Glu Leu
87 180 185 190
88 Lys Lys Ile Leu Asp Asp Trp Gly Glu Thr Cys Lys Gly Cys Ala Glu
89 195 200 205
90 Lys Ser Asp Tyr Ile Arg Lys Ile Asn Glu Leu Met Pro Lys Tyr Ala
91 210 215 220
92 Pro Lys Ala Ala Ser Ala Pro Thr Asp Leu
93 225 230
94 <210> SEQ ID NO: 3
95 <211> LENGTH: 179
96 <212> TYPE: PRT
97 <213> ORGANISM: human
98 <220> FEATURE:
99 <223> OTHER INFORMATION: amino acid sequence of human DG153 protein,
100 shorter variant
101 <400> SEQUENCE: 3
102 Met Trp Ala Thr Gln Gly Leu Ala Val Ala Leu Ala Ser Val Leu
103 1 5 10 15
104 Pro Gly Ser Arg Ala Leu Arg Pro Gly Asp Cys Glu Val Cys Ile Ser
105 20 25 30
106 Tyr Leu Gly Arg Phe Tyr Gln Asp Leu Lys Asp Arg Asp Val Thr Phe
107 35 40 45
108 Ser Pro Ala Thr Ile Glu Asn Glu Leu Ile Lys Phe Cys Arg Glu Ala

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131 50 55 60
 133 Arg Gly Lys Glu Asn Arg Leu Cys Tyr Tyr Ile Gly Ala Thr Asp Asp
 134 65 70 75 80
 136 Ala Ala Thr Lys Ile Ile Asn Glu Val Ser Lys Pro Leu Ala His His
 137 85 90 95
 139 Ile Pro Val Glu Lys Ile Cys Glu Lys Leu Lys Lys Asp Ser Gln
 140 100 105 110
 142 Ile Cys Glu Leu Lys Tyr Asp Lys Gln Ile Asp Leu Ser Thr Val Asp
 143 115 120 125
 145 Leu Lys Leu Arg Val Lys Glu Leu Lys Lys Ile Leu Asp Asp Trp
 146 130 135 140
 148 Gly Glu Thr Cys Lys Gly Cys Ala Glu Lys Ser Asp Tyr Ile Arg Lys
 149 145 150 155 160
 151 Ile Asn Glu Leu Met Pro Lys Tyr Ala Pro Lys Ala Ala Ser Ala Arg
 152 165 170 175
 154 Thr Asp Leu
 159 <210> SEQ ID NO: 4
 160 <211> LENGTH: 3714
 161 <212> TYPE: DNA
 162 <213> ORGANISM: human
 164 <220> FEATURE:
 165 <223> OTHER INFORMATION: nucleotide sequence of human DG177 protein
 167 <400> SEQUENCE: 4
 168 ggcacgaggg atcggcgagg ctccccaccc tcgttacagc tcgctgccgc cgtcctgccc 60
 169 cgcgccccca ggagacacctg accagaccac gatgtggaaa cgctggctcg cgctcgcgct 120
 170 cgcgctgggt gcggtcgcct gggtccgcgc cgaggaagag ctaaggagca aatccaagat 180
 171 ctgtgccaat gtgtttgtg gagccggccg ggaatgtgca gtcacagaga aaggggaaacc 240
 172 cacctgtctc tgcattgagc aatgcaaacc tcacaagagg cctgtgtgtg gcagtaatgg 300
 173 caágacctac ctcaaccact gtgaactgca tcgagatgcc tgcctcactg gatccaaaat 360
 174 ccaggttcat tacatggac actgcaaaga gaagaaatcc gtaagtccat ctgccagccc 420
 175 agttgttgc tatcaigtcca accgtgatga gctccgacgt cgcatcatcc agtggctgga 480
 176 agctgagatc attccagatg gctggttctc taaaggcagc aactacagtg aaatcctaga 540
 177 caagtatttt aagaactttg ataatggtga ttctcgctg gactccagtg aatcctgaa 600
 178 gtttgtggaa cagaatgaaa ctgccatcaa tattacaacg tatccagacc aggagaacaa 660
 179 caagttgctt aggggactct gtgttgcgtc tctcattgaa ctgtctgatg aaaatgctga 720
 180 ttggaaactc agcttccaag agtttctcaa gtgcctcaac ccattttca accctcctga 780
 181 gaagaagtgt gcccggagg atgaaacgta tgcagatgga gctgagaccc aggtggactg 840
 182 taaccgctgt gtctgtgcct gtggaaattt ggtctgtaca gccatgaccc gtgacggaaa 900
 183 gaatcagaag ggggcccaga cccagacaga ggaggagatg accagatatg tccaggagct 960
 184 ccaaaaagcat cagaaaaacag ctgaaaaagac caagagatg agcaccaaaag agatctaattg 1020
 185 aggaggcaca gaccagtgtc tggatccccat catttctcc acttcagccgc tgagttcagt 1080
 186 atacacaagt gtctgtacat gtcgccaat caccagtatt tgcttatata gcaatgagtt 1140
 187 ttatttgtt tattttgtt gcaataaaagg atatgaaggt ggctggctag gaagggaaagg 1200
 188 gcccacgcct tcatttcttag gagtgcctta agaaaaactg taaaatggtc tctggggctg 1260
 189 gaggcttagta aggaaaactgc atcacgattt aaagaggaaac agacccaaat ctgaacctct 1320
 190 tttgagttt ctgcattctgt cagcaggctg cagggagatgc acacgatgcc agagagaact 1380
 191 tagcagggtg tccccggagg agaggtttgg gaagctccac ggagaggaac gctctctgct 1440
 192 tccacgccttc ttccattgcc gtcagcatga cagacctcca gcatccacgc atctcttggt 1500
 193 cccaaataact gcctcttagat acatagccat actgctagtt aaccctcactg ccctcagact 1560

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250 Glu Pro Thr Cys Leu Cys Ile Glu Gln Cys Lys Pro His Lys Arg Pro
251 50 55 60
253 Val Cys Gly Ser Asn Gly Lys Thr Tyr Leu Asn His Cys Glu Leu His
254 65 70 75 80
256 Arg Asp Ala Cys Leu Thr Gly Ser Lys Ile Gln Val Asp Tyr Asp Gly
257 85 90 95
259 His Cys Lys Glu Lys Lys Ser Val Ser Pro Ser Ala Ser Pro Val Val
260 100 105 110
262 Cys Tyr Gln Ser Asn Arg Asp Glu Leu Arg Arg Arg Ile Ile Gln Trp
263 115 120 125
265 Leu Glu Ala Glu Ile Ile Pro Asp Gly Trp Phe Ser Lys Gly Ser Asn
266 130 135 140
268 Tyr Ser Glu Ile Leu Asp Lys Tyr Phe Lys Asn Phe Asp Asn Gly Asp
269 145 150 155 160
271 Ser Arg Leu Asp Ser Ser Glu Phe Leu Lys Phe Val Glu Gln Asn Glu
272 165 170 175
274 Thr Ala Ile Asn Ile Thr Thr Tyr Pro Asp Gln Glu Asn Asn Lys Leu
275 180 185 190
277 Leu Arg Gly Leu Cys Val Asp Ala Leu Ile Glu Leu Ser Asp Glu Asn
278 195 200 205
280 Ala Asp Trp Lys Leu Ser Phe Gln Glu Phe Leu Lys Cys Leu Asn Pro
281 210 215 220
283 Ser Phe Asn Pro Pro Glu Lys Lys Cys Ala Leu Glu Asp Glu Thr Tyr
284 225 230 235 240
286 Ala Asp Gly Ala Glu Thr Glu Val Asp Cys Asn Arg Cys Val Cys Ala
287 245 250 255
289 Cys Gly Asn Trp Val Cys Thr Ala Met Thr Cys Asp Gly Lys Asn Gln
290 260 265 270
292 Lys Gly Ala Gln Thr Gln Thr Glu Glu Glu Met Thr Arg Tyr Val Gln
293 275 280 285
295 Glu Leu Gln Lys His Gln Glu Thr Ala Glu Lys Thr Lys Arg Val Ser
296 290 295 300
298 Thr Lys Glu Ile
299 305
303 <210> SEQ ID NO: 6
304 <211> LENGTH: 26
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
311 <220> FEATURE:
312 <223> OTHER INFORMATION: mouse DG153 forward primer
314 <400> SEQUENCE: 6
315 agagaatcgg ttgtgctact acattg 26
318 <210> SEQ ID NO: 7
319 <211> LENGTH: 21
320 <212> TYPE: DNA
321 <213> ORGANISM: Artificial Sequence
323 <220> FEATURE:

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date